

In the specification:

[0100] Construction of a biased peptide library has been described previously. Martin et al., *J. Biol. Chem.* 271:361-366, 1996; Schatz et al., *Meth. Enzymol.* 267:171-191, 1996. The vector used for library construction was pJS142 (see Figure 2). This vector had a linker sequence between the LacI and the biased ~~undecamer~~ undecamer peptide coding sequence, as well as restriction sites for cloning the library oligonucleotide. The oligonucleotide synthesized to encode the mutagenesis library was synthesized with 70% of the correct base and 10% of each of the other bases at each position. This mutagenesis rate leads to a biased library such that there is approximately a 50% chance that any of the 11 codons will be the appropriate amino acid and approximately a 50% chance that it will be another amino acid. In addition, a linker of four random NNK (where N denotes A, C, G or T and K denotes G or T) codons were synthesized at the 5' end of the sequence to make a total of 15 randomized codons. Using this method, a library with greater than  $10^9$  independent clones per microgram of vector used in the ligation was constructed based on the carboxyl terminal sequence of G $\alpha$ t (IKENLKDCGLF; SEQ ID NO:139). The nucleic acid used for creating this library was 5'-GAGGTGGTNNKNNKNNKNNK~~at~~caaggagaaacctgaaggactgcggcctcttcTAACTAAGTAAAGC-3', wherein N= A/C/G/T and K= G/T; SEQ ID NO:140).